SEQUENCE LISTING

5	(1) GENERAL INFORMATION:
10	 (i) APPLICANT: (A) NAME: Boehringer Ingelheim International GmbH (B) STREET: Binger Strasse 173 (C) CITY: Ingelheim am Rhein (E) COUNTRY: Germany (F) POSTAL CODE (ZIP): 55216 (G) TELEPHONE: 06132/772282 (H) TELEFAX: 06132/774377
	(ii) TITLE OF INVENTION: Tumor Growth Inhibition- and Apoptosis-Associated Genes and Polypeptides and Methods of Use Thereof
20	(iii) NUMBER OF SEQUENCES: 24
25	<pre>(iv) COMPUTER READABLE FORM: (A) MEDIUM TYPE: Floppy disk (B) COMPUTER: IBM PC compatible (C) OPERATING SYSTEM: PC-DOS/MS-DOS (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)</pre>
30	(v) PRIOR APPLICATION DATA:(A) APPLICATION NUMBER: US 893 764(B) FILING DATE: 11-JUL-1997
35	(2) INFORMATION FOR SEQ ID NO:1:
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 549 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: both
45	(ii) MOLECULE TYPE: cDNA
	(ix) FEATURE: (A) NAME/KEY: CDS
50	(B) LOCATION: 1549

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15	TCT Ser										14	14
13	GCC Ala 50										15	92
20	AAT Asn										24	40
25	TAC Tyr										28	88
30	TGG Trp										33	36
35	ATT			•							38	84
33	CGG Arg	Ala									4:	32
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45	A AGC n Ser						Tyr				5:	28
50	GAA Glu			Arg							5	49

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5			(1) :	(B)	LEI TYI	NGTH PE: 8	: 182 amino	ERIS: 2 am: 5 ac: linea	ino a id		S					
10	·	•		MOLE(_			Q ID	NO:	2:				
15	1	٠.		Ala	. 5					10					15	
	Cys	ser	Pne	Ile 20	vai	PIO	Arg	ser	25	ırp	Arg	AIA	ьeu	30	ser	GIU
20	Cys	Ser	Ser 35	Arg	Leu	Gly	His	Pro 40	Val	Arg	Tyr	Val	Val 45	Ile	Ser	His
	Thr	Ala 50	Gly	Ser	Phe	Cys	Asn 55	Ser	Pro	Asp	Ser	Cys 60	Glu	Gln	Gln	Ala
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	Gly	Trp	Asn	Ile 100	Lys	Gly	Asp	His	Thr 105	Gly	Pro	Ile	Trp	Asn 110	Pro	Met
35	Ser	Ile	Gly 115	Ile	Thr	Phe		Gly 120	Asn	Phe	Met	Asp	Arg 125	Val	Pro	Ala
	Lys	Arg 130	Ala	Leu	Arg	Ala	Ala 135	Leu	Asn	Leu	Leu	Glu 140	Cys	Gly	Val	Ser
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45	Gln	Ser	Thr	Leu	Ser 165	Pro	Gly	Asp	Gln	Leu 170	Tyr	Gln	Val	Ile	Gln 175	Ser
	Trp	Glu	His	Tyr 180	Arg	Glu									•	

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	(ii)	MOLECULE TYPE:	cDNA to mRNA	L		
10	(iii)	HYPOTHETICAL: N	0			
	(iv)	ANTI-SENSE: NO				•
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40	CCGCTCT	ATG CTG CTT GCC Met Leu Leu Ala 1				109
45		CAG GAG ACA GAA Gln Glu Thr Glu 20				157
50		GAG TGG AAG GCC Glu Trp Lys Ala 35				205
EE		TTA CGC TAT GTG Leu Arg Tyr Val 50				253
55		CCC GCC TCG TGC Pro Ala Ser Cys 65			Gln His Tyr	301

5	CAC ATG AAG ACA CTG GGC TGG TGC GAC GTG GGC THIS Met Lys Thr Leu Gly Trp Cys Asp Val Gly T	TAC AAC TTC CTG ATT 34 Tyr Asn Phe Leu Ile 90	49
3	GGA GAA GAC GGG CTC GTA TAC GAG GGC CGT GGC 1 Gly Glu Asp Gly Leu Val Tyr Glu Gly Arg Gly 1 95 100 105	IGG AAC TTC ACG GGT 39 Trp Asn Phe Thr Gly 110	97
10	GCC CAC TCA GGT CAC TTA TGG AAC CCC ATG TCC F Ala His Ser Gly His Leu Trp Asn Pro Met Ser I 115 120	ATT GGC ATC AGC TTC 44 Lie Gly Ile Ser Phe 125	45
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20	GCC CAG GGT CTA CTG GCC TGC GGT GTG GCT CAG G Ala Gln Gly Leu Leu Ala Cys Gly Val Ala Gln G 145 150	GGA GCC CTG AGG TCC 54 Gly Ala Leu Arg Ser 155	41
25	AAC TAT GTG CTC AAA GGA CAC CGG GAT GTG CAG C Asn Tyr Val Leu Lys Gly His Arg Asp Val Gln A 160 165 1	CGT ACA CTC TCT CCA 58 Arg Thr Leu Ser Pro .70	89
	GGC AAC CAG CTC TAC CAC CTC ATC CAG AAT TGG C Gly Asn Gln Leu Tyr His Leu Ile Gln Asn Trp F 175 180 185	CCA CAC TAC CGC TCC 63 Pro His Tyr Arg Ser 190	37
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45	(D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein		
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	10	Asp	Gly	Leu	Val 100	Tyr	Glu	Gly	Arg	Gly 105	Trp	Asn	Phe	Thr	Gly 110	Ala	His
	15	Ser	Gly	His 115	Leu	Trp	Asn	Pro	Met 120	Ser	Ile	Gly	Ile	Ser 125	Phe	Met	Gly
		Asn	Tyr 130	Met	Asp	Arg	Val	Pro 135		Pro	Gln	Ala	Ile 140	Arg	Ala	Ala	Gln
	20	Gly 145	Leu	Leu	Ala	Cys	Gly 150	Val	Ala	Gln	Gly	Ala 155	Leu	Arg	Ser	Asn	Tyr 160
	25	Val	Leu	Lys	Gly	His 165	Arg	Asp	Val	Gln	Arg 170	Thr	Leu	Ser	Pro	Gly 175	Asn
	23	Gln	Leu	Tyr	His 180	Leu	Ile	Gln	Asn	Trp 185	Pro	His	Tyr	Arg	Ser 190	Pro	*
	30						-		-								
		(2)	INI	FORM	OITA	v FOI	R SE	Q ID	NO:	5 :							
	35		(i)	() ()	A) L1 3) Ti C) Si	engti YPE : Trani	HARAC H: 14 nuc: DEDNI DGY:	l bas leic ESS:	se pa acio sing	airs 1							
	40		(ii)				YPE:			ic D	NA.						
			(xi)) SE(QUEN	CE DI	ESCR:	[PTIC	ON: S	SEQ :	ID N	0:5:					
	45	TTTT	rttt'	rtt :	TTAC												14
	50	(2)	INFO	ORMA:	rion	FOR	SEQ	ID I	10 : 6	:							
	55		(i)	() ()	A) L1 B) T1 C) S1	engti YPE : Trani	HARAG H: 10 nucl DEDNI	bas leic ESS:	se pa acio sino	airs 1							

		(ii) MOLECULE TYPE: synthetic DNA	
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	20	(ii) MOLECULE TYPE: synthetic DNA	
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Trada Chara	25	AGTCAGCCAC	10
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		(ii) MOLECULE TYPE: synthetic DNA	
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		GGCCGCTAGC CTGCAGTTAT CACTCTCGGT AGTGTTCCCA G	41
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		V-	

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드 주 투	20	(ii) MOLECULE TYPE: synthetic DNA	
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7	15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 31 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
ոոր Կուս. ուրք 11 Ո Կույն Աոգի	20	(ii) MOLECULE TYPE: synthetic DNA	
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		(ii) MOLECULE TYPE: synthetic DNA	
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		(ii) MOLECULE TYPE: protein	

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5	Arg Ser Glu Trp Arg Ala Leu Pro Ser Glu Cys Ser Ser Arg Leu Gly 1 5 10 15
	His Pro Tyr
10	
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20	(ii) MOLECULE TYPE: protein
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	Gly Glu Asp Gly His Val Tyr Glu Gly Arg Gly Trp Asn Ile Lys Gly 1 5 10 15
30	Asp His Thr Gly Cys Tyr 20
35	(2) INFORMATION FOR SEQ ID NO:23:
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40	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: protein
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1)

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10	(ii) MOLECULE TYPE: protein
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:
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514 Rec'd PO 1 1 JAN 2000

-1-

SEQUENCE LISTING

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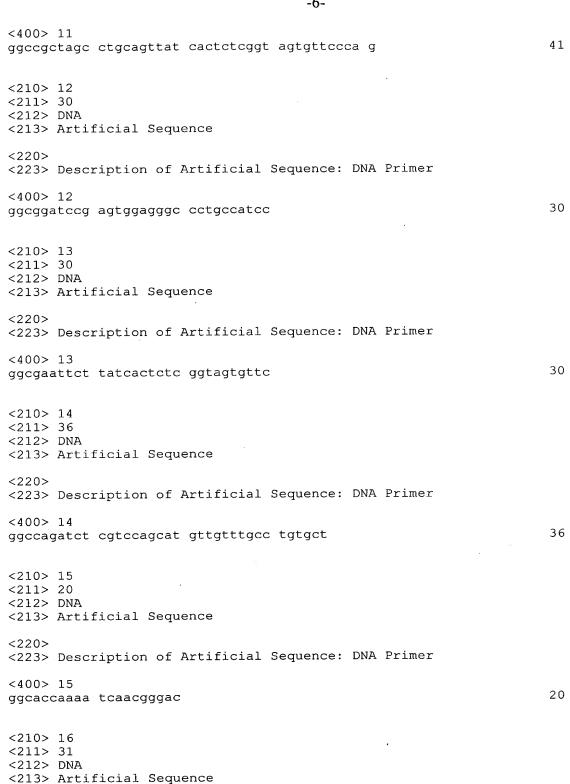
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Leu Pro Leu Arg Tyr Val Val Val Ser His Thr Ala Gly Ser Ser Cys
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                                                             110
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31

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